ISMRM 2006 Educational Lecture

Measuring Brain Volume Changes: The Tools

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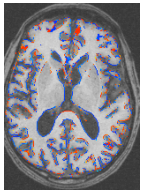
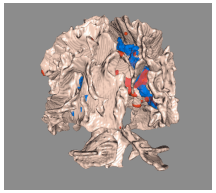
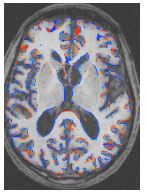




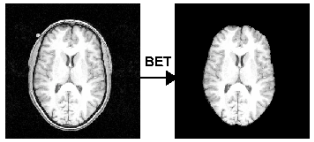
Measuring Brain Volume Changes: The Tools

- Tissue-type segmentation & bias field correction
- Longitudinal: temporal brain change
- Cross-sectional: single time point brain state
- Localised analyses

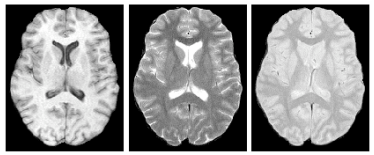


Segmentation example: FAST from FSL

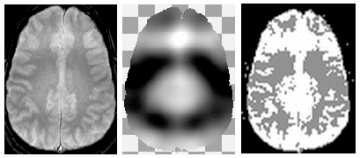
- First use BET to remove non-brain



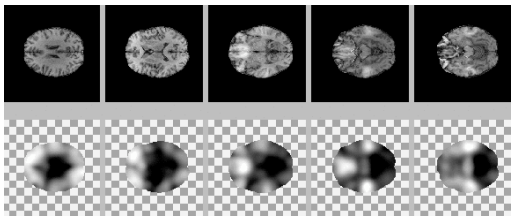
- Input can be single image (e.g. T1, T2, Proton Density)
- Or several of these ("multi-channel")
- For multi-channel, all must be aligned (e.g. with FLIRT)



MR Images - RF Inhomogeneity ("Bias Field")

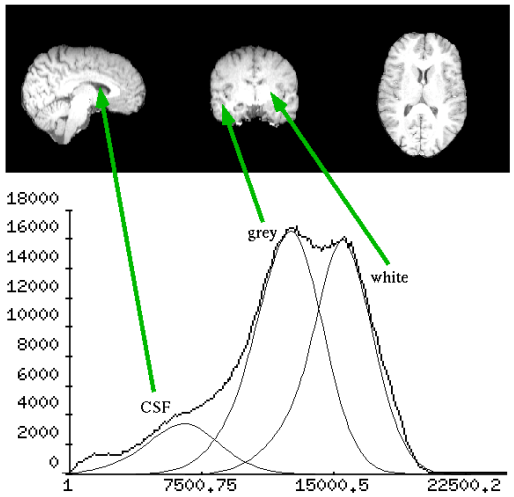


- RF Inhomogeneity causes intensity variations in image
- Causes problems for simple threshold-based segmentation
- Need to remove bias field before or within segmentation



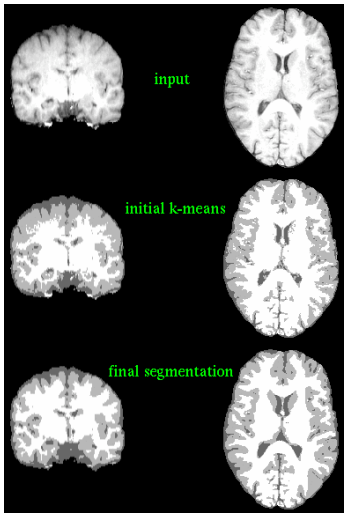
Histograms - Tissue Intensity Distributions

- Histogram = "voxel count vs intensity"
- Mixture of Gaussians
- Model class means and widths
- If well separated, clear peaks, i.e. segmentation easy
- But overlap worsened by: bias, blurring, low resolution, head motion



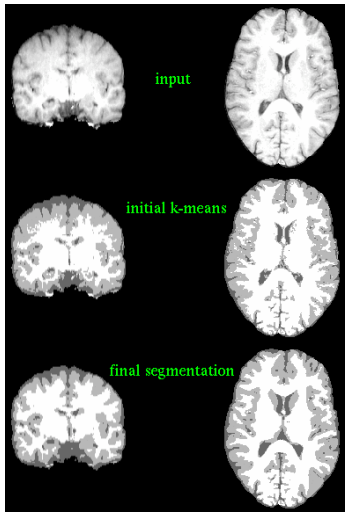
Initial Segmentation

- Need to bootstrap method somehow - initial segmentation
- Use "Tree-Structure K Means"
- Start with one class (Gaussian)
- Split & fit
- Re-split until enough classes
- Many other segmentations **only** do this step!



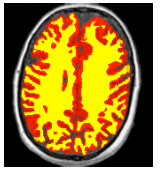
Using Spatial Neighbourhood Information (MRF)

- Neighbourhood information: "if my neighbours are grey matter then I probably am too"
- Most methods (like the k-means initialisation) don't use spatial neighbourhood information
- Reduces noise and increases robustness
- Carried out using MRF (Markov Random Field) model



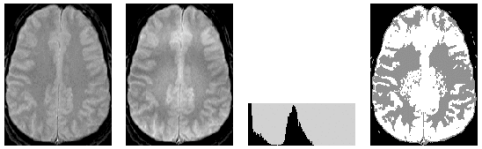
At Last - the Overview!

- Initial segmentation - tree-structure k-means
- Iterate
  - Estimate bias field
  - Iterate segmentation
    - Update segmentation
    - Update tissue class parameters (mean and standard deviation)

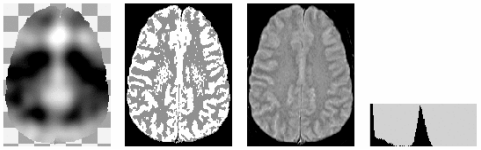


Examples - Single Channel Segmentation

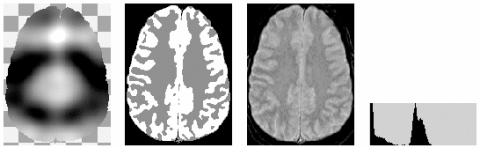
Original,
original plus bias field,
histogram,
best thresholding
segmentation



No MRF used:
estimated bias,
segmentation, restored
image, histogram

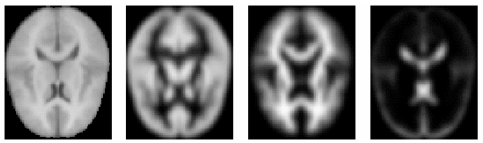


With MRF



A-Priori Tissue Probability Maps

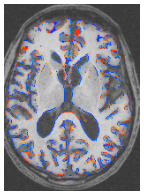
- A-priori maps created by averaging many aligned segmentations; can be used as priors in segmentation but can skew results
- If bias is very bad, priors can aid initial segmentation
- A-priori maps can also be optionally used to feed into final posteriors (e.g. to aid segmentation of deep gray); FAST doesn't use this by default, SPM2 does
- SPM5 improves the use of priors (compared with SPM2) by combining segmentation with alignment to priors.



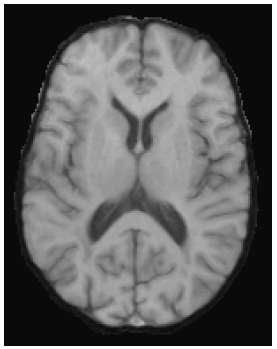
Longitudinal Change Analysis

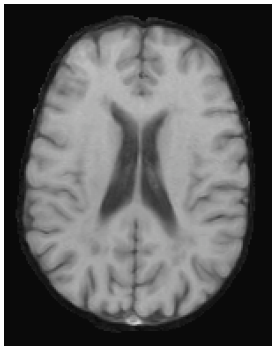
Example: SIENA (Structural Image Evaluation, using Normalisation, of Atrophy, from FSL)

- Measures atrophy / general brain change
- Accurate and fully automatic
- Proven for a range of slice thicknesses
- Proven for a range of MRI sequences
- Accuracy 0.2% of brain volume
- Correction for scanner geometry drifts



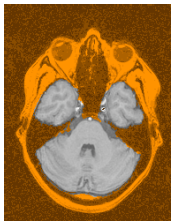
Example of Atrophy in Action





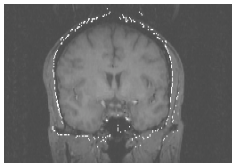
BET : Brain Extraction Tool

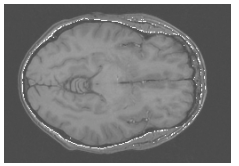
- Eliminates all non-brain tissue
- Accurate and fully automatic
- < 1 minute processing time

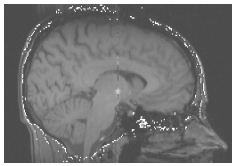


BET : Brain Extraction Tool

- Estimation of exterior surface of skull
- Used to hold image scale constant in registration

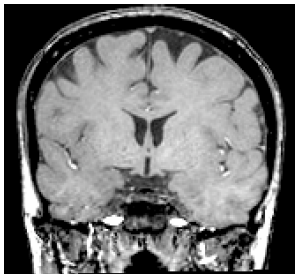






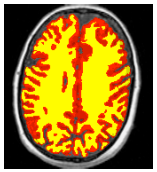
FLIRT Linear Registration

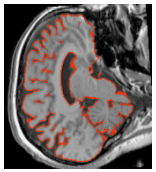
- Register brains (full affine)
- Apply to skulls then re-register skulls, altering only scale and skew (corrects for changes in scanner geometry etc.)
- Apply to brains then re-optimise rotation and translation
- Use transform's midway position
- < 10 minutes for 3-step registration

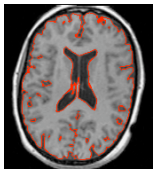


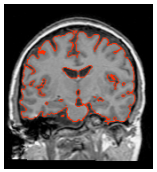
Atrophy Measurement Using Edge Motion

Find brain/non-brain edge points in image 1 using FAST tissue
segmentation (including bias-field correction)



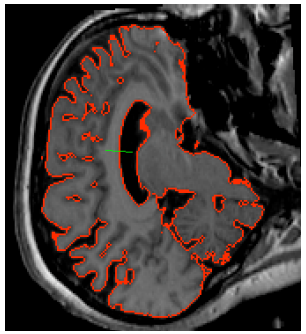


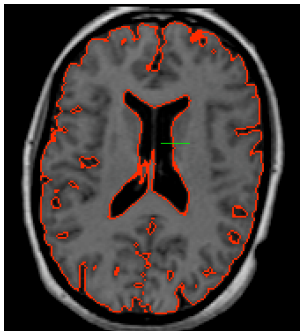




Atrophy Measurement Using Edge Motion

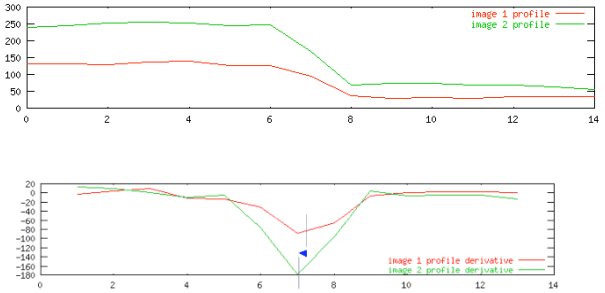
At each edge point take 1D perpendicular profile





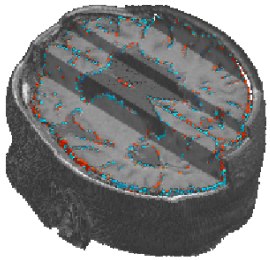
Atrophy Measurement Using Edge Motion

- Find profile from same point in image 2
- Take windowed derivative of both
- Correlate with subvoxel accuracy



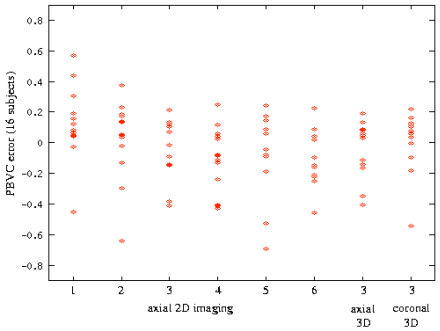
Atrophy Measurement Using Edge Motion

- Thus for each edge point in image 1 the perpendicular motion is found
- Insensitive to changes in imaging
- Mean motion over whole brain surface calculated
- Convert into % brain volume change (PBVC) by estimating brain surface area and volume and then doing self-calibration
- Example: blue=atrophy, red="growth"



Error Plots from "Normals"

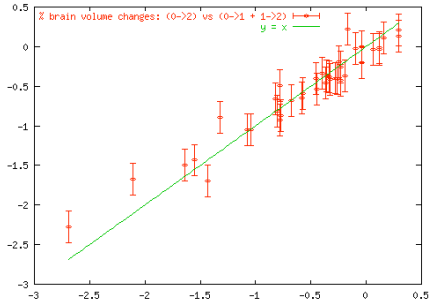
- 16 normals, each scanned twice
- Range of slice thicknesses
- Error not dependent on slice thickness
- Error approximately 0.2%



Error Plots from 3 Time Points from Patients

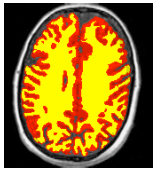
Data courtesy of V. Stevenson, D. Miller *et al.*, ION, London

- 39 patients (white-matter atrophy)
- Three time points
- Test accuracy by
  t0->t2
  vs
  t0->t1 + t1->t2
- Errors within 0.2%



Cross-Sectional Atrophy: Brain State

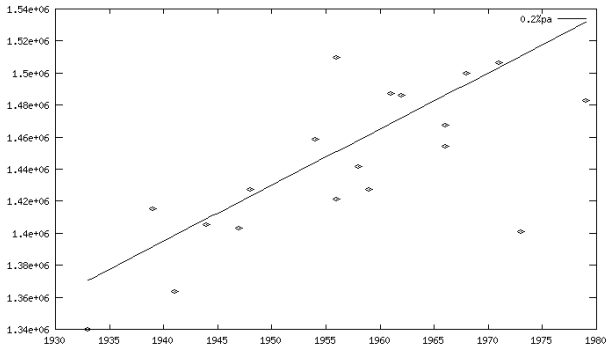
- Example: SIENAX (from FSL)
- Measures brain volume normalised for head size
- Proven for T1, T2, PD etc.
- Test-retest error 0.5-1% (0.2-0.4% without normalisation)
- SE for normals 0.7% (1.5% without normalisation)



SIENAX : Cross-Sectional Atrophy

- BET: find brain and skull
- FLIRT: use brain & skull to normalise to standard space
- Use standard space mask to cut brain stem and ensure no optic nerve/eyeballs
- Tissue segmentation (FAST, including partial volume estimation)
- Gives (normalised) brain (and grey & white) volume

Normalised Brain Volume vs DoB (Normals)



SIENAX Results : MS vs Controls

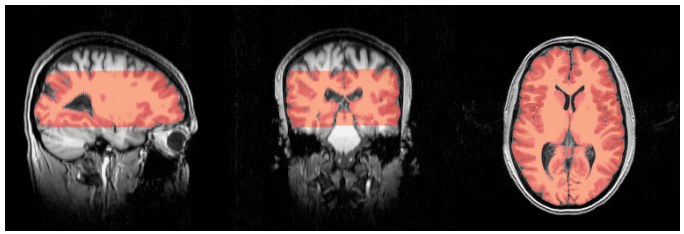
Group	N	Mean Volume /10^6 mm^3	SD /10^6 mm^3	P
Controls	20	1.45	0.05	
Total MS	72	1.39	0.10	0.0001
EDSS <2	33	1.44	0.07	
EDSS <5	61	1.41	0.09	0.01
EDSS 2-4	27	1.38	0.10	0.0001
EDSS 5-8	10	1.27	0.10	0.0001

- Data from Siena, Italy
- ANOVA Tukey shows significant difference between controls and all EDSS bins except for EDSS<2

Cross-Subject Comparisons (Partial Head Images)

If different subjects have varying amounts of head in field of view, atrophy comparisons are not valid. Therefore use standard-space-based masking or Z limits so that all is consistent.

For example, to only use data where
-20mm < Z < +50mm (in standard space),
use options `-b -20 -t 50`



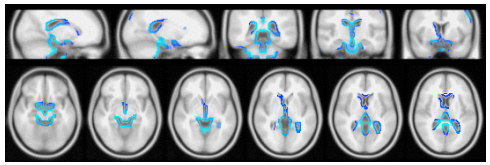
Voxelwise Cross-Subject Statistics - SIENAr

Extend SIENA for voxelwise cross-subject statistics, e.g.:

- where is atrophy different between two groups,
- or where does atrophy correlate with EDSS

- run SIENA to get edge "flow" image
- dilate
- transform to standard space
- mask with standard-space edge-mask
- blur (optional)
- carry out voxelwise cross-subject statistics

Voxelwise Cross-Subject Statistics - SIENAr

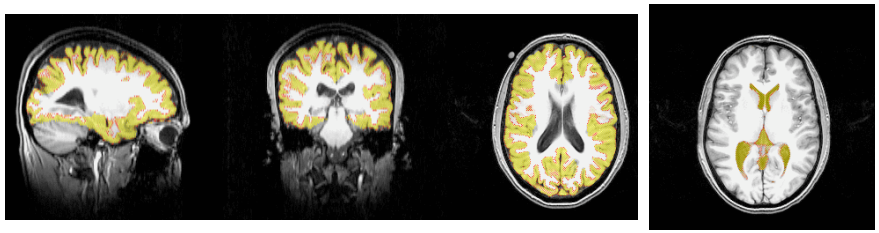


Example - one-group MS atrophy

Regional Atrophy Measurement - SIENAX

With SIENAX, carry out regional breakdown

This gives peripheral GM volume and ventricular CSF volume, using standard-space masks.



Voxelwise Volumetry - VBM

- VBM: Voxelwise structural stats, e.g. with SPM or SIENAX+IRTK(nonlinear reg):

- Segment -> GM PVE
- Align to standard space (with density modulation)
- Voxelwise cross-subject stats

- Pros: fully automated, easy to test whole brain
- Con: ambiguity between cross-subject geometry shifts and intensity changes...hard to interpret results sometimes

References

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